

Sequence length 4052

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TGGTCTCGAAGAAGCCCGTGCCTGTTTAAAACTGATCCTAACTAAAAACAGACTTGAGTGGAT	M R M L	4
	ATG AGA ATG TTG	12
V S G R R V K K W Q L I I Q L F A T C F		24
GTT AGT GGC AGA AGA GTC AAA AAA TGG CAG TTA ATT ATT CAG TTA TTT GCT ACT TGT TTT		72
L A S L M F F W E P I D N H I V S H M K		44
TTA GCG AGC CTC ATG TTT TTT TGG GAA CCA ATC GAT AAT CAC ATT GTG AGC CAT ATG AAG		132
S Y S Y R Y L I N S Y D F V N D T L S L		64
TCA TAT TCT TAC AGA TAC CTC ATA AAT AGC TAT GAC TTT GTG AAT GAT ACC CTG TCT CTT		192
K H T S A G P R Y Q Y L I N H K E K C Q		84
AAG CAC ACC TCA GCG GGG CCT CGC TAC CAA TAC TTG ATT AAC CAC AAG GAA AAG TGT CAA		252
A Q D V L L L L F V K T A P E N Y D R R		104
GCT CAA GAC GTC CTC CTT TTA CTG TTT GTA AAA ACT GCT CCT GAA AAC TAT GAT CGA CGT		312
S G I R R T W G N E N Y V R S Q L N A N		124
TCC GGA ATT AGA AGG ACG TGG GGC AAT GAA AAT TAT GTT CGG TCT CAG CTG AAT GCC AAC		372
I K T L F A L G T P N P L E G E E L Q R		144
ATC AAA ACT CTG TTT GCC TTA GGA ACT CCT AAT CCA CTG GAG GGA GAA GAA CTA CAA AGA		432
K L A W E D Q R Y N D I I Q Q D F V D S		164
AAA CTG GCT TGG GAA GAT CAA AGG TAC AAT GAT ATA ATT CAG CAA GAC TTT GTT GAT TCT		492
F Y N L T L K L L M Q F S W A N T Y C P		184
TTC TAC AAT CTT ACT CTG AAA TTA CTT ATG CAG TTC AGT TGG GCA AAT ACC TAT TGT CCA		552
H A K F L M T A D D D I F I H M P N L I		204
CAT GCC AAA TTT CTT ATG ACT GCT GAT GAT GAC ATA TTT ATT CAC ATG CCA AAT CTG ATT		612
E Y L Q S L E Q I G V Q D F W I G R V H		224
GAG TAC CTT CAA AGT TTA GAA CAA ATT GGT GTT CAA GAC TTT TGG ATT GGT CGT GTT CAT		672
R G A P P I R D K S S K Y Y V S Y E M Y		244
CGT GGT GCC CCT CCC ATT AGA GAT AAA AGC AGC AAA TAC TAC GTG TCC TAT GAA ATG TAC		732
Q W P A Y P D Y T A G A A Y V I S G D V		264
CAG TGG CCA GCT TAC CCT GAC TAC ACA GCC GGA GCT GCC TAT GTA ATC TCC GGT GAT GTA		792
A A K V Y E A S Q T L N S S L Y I D D V		284
GCT GCC AAA GTC TAT GAG GCA TCA CAG ACA CTA AAT TCA AGT CTT TAC ATA GAC GAT GTG		852

Fig. 1A

F	M	G	L	C	A	N	K	I	G	I	V	P	Q	D	H	V	F	F	S	304
TTC	ATG	GGC	CTC	TGT	GCC	AAT	AAA	ATA	GGG	ATA	GTA	CCG	CAG	GAC	CAT	GTG	TTT	TTT	TCT	912
G	E	G	K	T	P	Y	H	P	C	I	Y	E	K	M	M	T	S	H	G	324
GGA	GAG	GGT	AAA	ACT	CCT	TAT	CAT	CCC	TGC	ATC	TAT	GAA	AAA	ATG	ATG	ACA	TCT	CAT	GGA	972
H	L	E	D	L	Q	D	L	W	K	N	A	T	D	P	K	V	K	T	I	344
CAC	TTA	GAA	GAT	CTC	CAG	GAC	CTT	TGG	AAG	AAT	GCT	ACA	GAT	CCT	AAA	GTA	AAA	ACC	ATT	1032
S	K	G	F	F	G	Q	I	Y	C	R	L	M	K	I	I	L	L	C	K	364
TCC	AAA	GGT	TTT	TTT	GGT	CAA	ATA	TAC	TGC	AGA	TTA	ATG	AAG	ATA	ATT	CTC	CTT	TGT	AAA	1092
I	S	Y	V	D	T	Y	P	C	R	A	A	F	I	*						379
ATT	AGC	TAT	GTG	GAC	ACA	TAC	CCT	TGT	AGG	GCT	GCG	TTT	ATC	TAA						1137

TAGTACTTGAATGTTGTATGTTTTCACCTGTCACCTGAGTCAAACCTGGATGAAAAAACCTTTAAATGTTTCGTCTATACC
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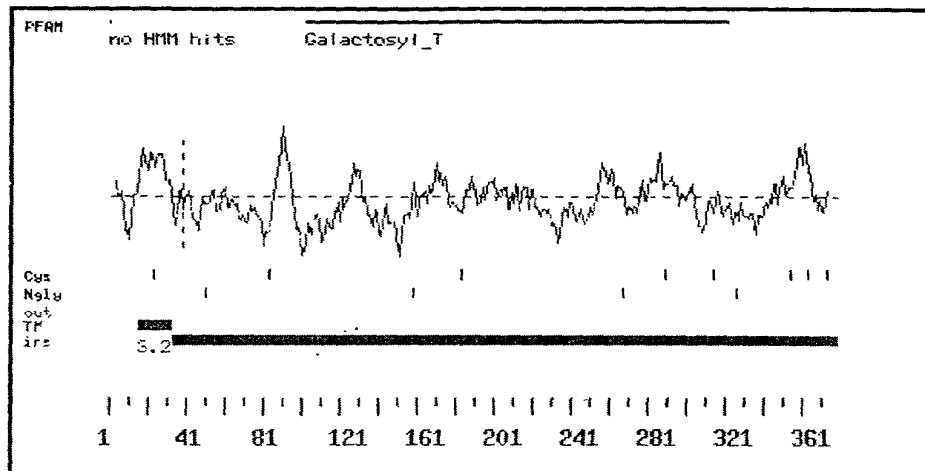
Fig. 1B

ACTACAGTGTCAAACATTCTAGGTTGTAGTTACTTTCAGAGTAGATACAGGGTTTTAGATCATTACAGTTTAAGTTTTCT
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GATTAATGATGTATTGCCTTTTGCCCATATATACCCTGTGTATCTATACTTGGAAGTGT'TAAGGTTGCCATTGGTTGA
AAACATAAGTGTCTCTGGCCATCAAAGTGATCTTGTTTACAGCAGTGCTTTTGTGAAACAATTATTTATTTGCTGAAAG
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TTGAATTTTGCTCTTGTATGGCAAAATAATTAGTGAGTTTAAAAAAAATCTATAGTTTCCAATAAACAACTGAAAAATT
AAAAAAA

03424101-4525466

Fig. 1C

Analysis of 8797 (378 aa)



>8797

MRMLVSGRRVKKWQLIIQLFATCFLASLMFFWEPIDNHIVSHMKSSYRYLINSYDFVND
 TSLKHTSAGPRYQYLINHKCKQAQDVLLLLFVKTAPENYDRRSGIRRTWGNENYVRSQ
 LNANIKTLFALGTPNPLEGEELQRKLAWEDQRYNDIIQQDFVDSFYNLTLKLLMQFSWAN
 TYCPHAKFLMTADDDIFIHMPNLIEYLSLEQIGVQDFWIGRVHRGAPPIRDKSSKYYVS
 YEMYQWPAYPDYTAGAAYVISGDVAAKVYEASQTLNSSLYIDDVFMGLCANKIGIVPQDH
 VFFSGEGKTPYHPCIEKMMTSHGHLEDLQDLWKNATDPKVKTIISKGFFGQIYCRMKII
 LLCKISYVDITYPCRAAFI

Fig. 2

Protein Family / Domain Matches, HMMer version 2

Searching for complete domains in PFAM

hmmfam - search a single seq against HMM database

HMMER 2.1.1 (Dec 1998)

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HMMER is freely distributed under the GNU General Public License (GPL).

HMM file: /prod/ddm/seqanal/PFAM/pfam5.4/Pfam
Sequence file: /prod/ddm/wspace/orfanal/oa-script.19955.seq

Query: 8797

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
Galactosyl_T	Galactosyltransferase	173.8	2.8e-48	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
Galactosyl_T	1/1	102	321	..	1 249 []	173.8	2.8e-48

Alignments of top-scoring domains:

Galactosyl_T: domain 1 of 1, from 102 to 321: score 173.8, E = 2.8e-48

```

      *->arRnaiRkTWmnqnnsevadgrikalFlvGl.sakgdqklklvme
8797  102  DRRSGIRRTWGNENYVRSQNLNANIKTLFALGTpNPLEGEELQRKLAW 148

      EakrtlyGDiiivvDleDsYenLtlKTLtilllygvskcpsakligKiDdDv
      E++  y Dii++D+ Ds++nLtlK 1+ ++++++cp+ak+ + DdD+
8797  149  EDQ--RYNDIIQQDFVDSFYNLTLKLLMQFSWANTYCPHAKFLMTADDDI 196

      fvnpgkLlslLereniridpsessfyGyiikegepvrrkkskrdWYvppt
      f+ +++L+++L+ i +++++ G++++ +p+r k sk Yv+++
8797  197  FIHMPNLIEYLQSL-EQIGVQDFWI-GRVHRGAPPIRDKSSK--YYVSYE 242

      eYpcsrNgnkYppYvsGpfYllsrdAAplIlkaskhrLr.flkiEDVliT
      Y + YP Y +G Y++s+d+A ++++as + ++ l i+DV++
8797  243  MYQWPA----YPDYTAGAAYVISGDVAAKVYEASQTL-NsSLYIDDVFM- 286

      GilaedlgIsrinlprlsistnlfrfhhsqkdndgcdvfawhtahkndpe
      G +a+++gI +++ +f++ +++ h++ +e
8797  287  GLCANKIGIVPQDH-----VFFSGEGKTPY-----HPCIYE 317

      ylif<-*
      ++ +
8797  318  KMMT 321
  
```

Fig. 3

Transmembrane Segments Predicted by MEMSAT

Start	End	Orient	Score
15	32	out-->ins	3.2

>8797

MRMLVSGRRVKKWQLIIQLFATCFLASLMFFWEPIDNHIVSHMKSSYSRYLINSYDFVND
 TSLKHTSAGPRYQYLINHKEKCQAQDVLLLLFVKTAPENYDRSGIRRTWGNENYVRSQ
 LNANIKTLFALGTPNPLEGEELQRKLAWEDQRYNDIIQQDFVDSFYNLTLKLLMQFSWAN
 TYCPHAKFLMTADDDIFIHMPNLIEYLOSLEQIGVQDFWIGRVHRGAPPIRDKSSKYYVS
 YEMYQWPAYPDYTAGAAYVISGDVAAKVYEASQTLNSSLYIDDVFMGLCANKIGIVPQDH
 VFFSGEGKTPYHPCIYEKMMTSHGHLEDLQDLWKNATDPKVKTISKGFFGQIYCRMKII
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Fig. 4

094544-033101

Fig. 5

T0T20" + 5254660

Phase 1.3.3 Expression of 8797 w/S2

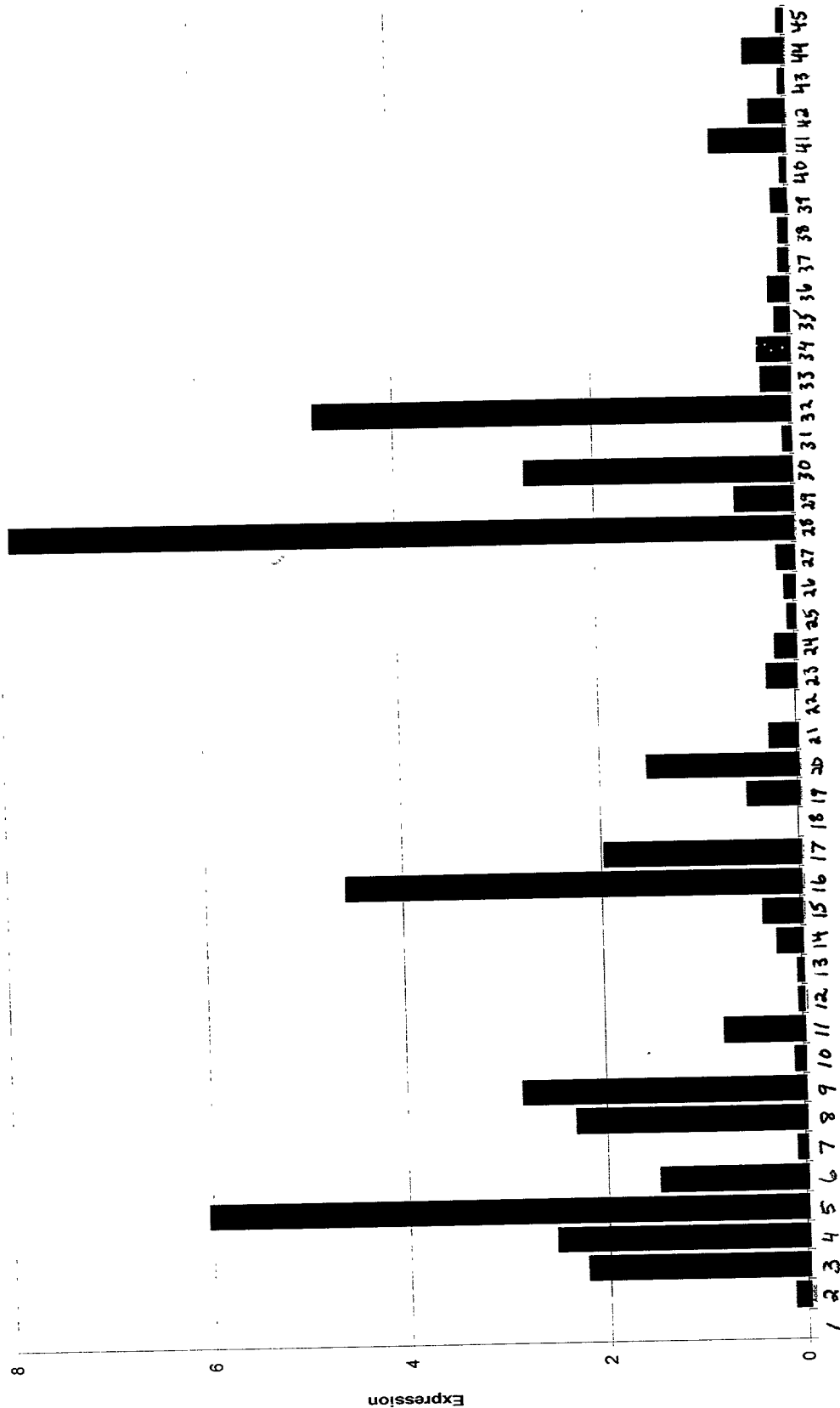
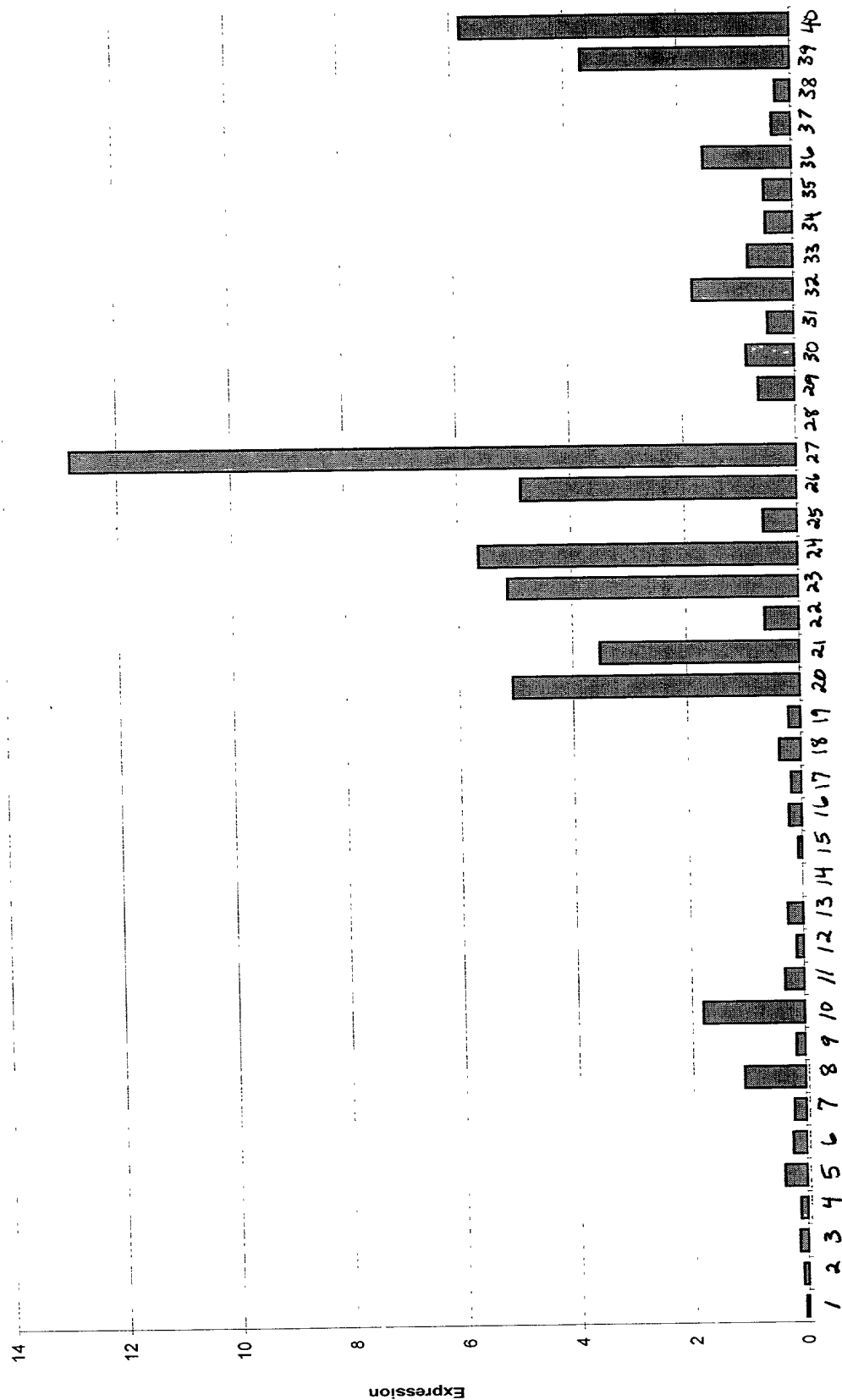


Fig. 6

FOIEEO 45254660

8797 Expression in Oncology Phase II Plate



1000045254650

Fig. 7

8797 Expression in Lung Model Panel

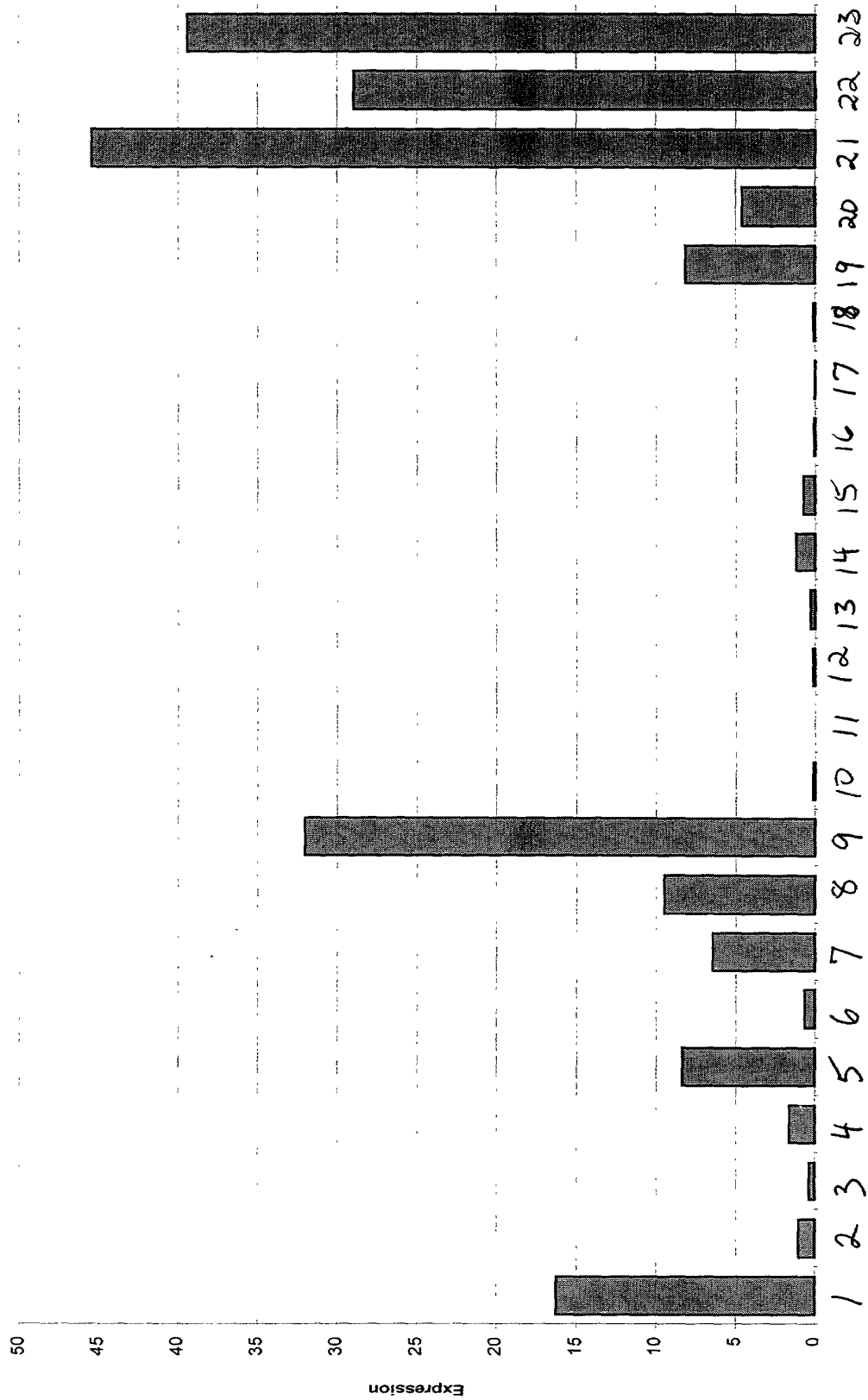


Fig. 8

FOIEB0 45254650

8797 Expression in the Breast Models Panel

